

Figure 1 (A)

GAATTCGGCTTCCATCCTAATACGACTCACTATAGGGCTCGAGCGGCCGCCGGGGCAGGTATCTTGGCTCACAGGGGA																				79
M	S	S	S	S	S	W	L	L	L	S	L	V	A	V	T	A	A	Q	S	19
CG	ATG	TCA	AGC	TCT	TCC	TGG	CTC	CTT	CTC	AGC	CTT	GTT	GCT	GTA	ACT	GCT	GCT	CAG	TCC	138
T	I	E	E	Q	A	K	T	F	L	D	K	F	N	H	E	A	E	D	L	39
ACC	ATT	GAG	GAA	CAG	GCC	AAG	ACA	TTT	TTG	GAC	AAG	TTT	AAC	CAC	GAA	GCC	GAA	GAC	CTG	198
F	Y	Q	S	S	L	A	S	W	N	Y	N	T	N	I	T	E	E	N	V	59
TTC	TAT	CAA	AGT	TCA	CTT	GCT	TCT	TGG	AAT	TAT	AAC	ACC	AAT	ATT	ACT	GAA	GAG	AAT	GTC	258
Q	N	M	N	N	A	G	D	K	W	S	A	F	L	K	E	Q	S	T	L	79
CAA	AAC	ATG	AAT	AAT	GCT	GGG	GAC	AAA	TGG	TCT	GCC	TTT	TTA	AAG	GAA	CAG	TCC	ACA	CTT	318
A	Q	M	Y	P	L	Q	E	I	Q	N	L	T	V	K	L	Q	L	Q	A	99
GCC	CAA	ATG	TAT	CCA	CTA	CAA	GAA	ATT	CAG	AAT	CTC	ACA	GTC	AAG	CTT	CAG	CTG	CAG	GCT	378
L	Q	Q	N	G	S	S	V	L	S	E	D	K	S	K	R	L	N	T	I	119
CTT	CAG	CAA	AAT	GGG	TCT	TCA	GTG	CTC	TCA	GAA	GAC	AAG	AGC	AAA	CGG	TTG	AAC	ACA	ATT	438
L	N	T	M	S	T	I	Y	S	T	G	K	V	C	N	P	D	N	P	Q	139
CTA	AAT	ACA	ATG	AGC	ACC	ATC	TAC	AGT	ACT	GGA	AAA	GTT	TGT	AAC	CCA	GAT	AAT	CCA	CAA	498
E	C	L	L	L	E	P	G	L	N	E	I	M	A	N	S	L	D	Y	N	159
GAA	TGC	TTA	TTA	CTT	GAA	CCA	GGT	TTG	AAT	GAA	ATA	ATG	GCA	AAC	AGT	TTA	GAC	TAC	AAT	558
E	R	L	W	A	W	E	S	W	R	S	E	V	G	K	Q	L	R	P	L	179
GAG	AGG	CTC	TGG	GCT	TGG	GAA	AGC	TGG	AGA	TCT	GAG	GTC	GGC	AAG	CAG	CTG	AGG	CCA	TTA	618
Y	E	E	Y	V	V	L	K	N	E	M	A	R	A	N	H	Y	E	D	Y	199
TAT	GAA	GAG	TAT	GTG	GTC	TTG	AAA	AAT	GAG	ATG	GCA	AGA	GCA	AAT	CAT	TAT	GAG	GAC	TAT	678
G	D	Y	W	R	G	D	Y	E	V	N	G	V	D	G	Y	D	Y	S	R	219
GGG	GAT	TAT	TGG	AGA	GGA	GAC	TAT	GAA	GTA	AAT	GGG	GTA	GAT	GGC	TAT	GAC	TAC	AGC	CGC	738
G	Q	L	I	E	D	V	E	H	T	F	E	E	I	K	P	L	Y	E	H	239
GGC	CAG	TTG	ATT	GAA	GAT	GTG	GAA	CAT	ACC	TTT	GAA	GAG	ATT	AAA	CCA	TTA	TAT	GAA	CAT	798
L	H	A	Y	V	R	A	K	L	M	N	A	Y	P	S	Y	I	S	P	I	259
CTT	CAT	GCC	TAT	GTG	AGG	GCA	AAG	TTG	ATG	AAT	GCC	TAT	CCT	TCC	TAT	ATC	AGT	CCA	ATT	858
G	C	L	P	A	H	L	L	G	D	M	W	G	R	F	W	T	N	L	Y	279
GGA	TGC	CTC	CCT	GCT	CAT	TTG	CTT	GGT	GAT	ATG	TGG	GGT	AGA	TTT	TGG	ACA	AAT	CTG	TAC	918
S	L	T	V	P	F	G	Q	K	P	N	I	D	V	T	D	A	M	V	D	299
TCT	TTG	ACA	GTT	CCC	TTT	GGA	CAG	AAA	CCA	AAC	ATA	GAT	GTT	ACT	GAT	GCA	ATG	GTG	GAC	978
Q	A	W	D	A	Q	R	I	F	K	E	A	E	K	F	F	V	S	V	G	319
CAG	GCC	TGG	GAT	GCA	CAG	AGA	ATA	TTC	AAG	GAG	GCC	GAG	AAG	TTT	TTT	GTA	TCT	GTT	GGT	1038
L	P	N	M	T	Q	G	F	W	E	N	S	M	L	T	D	P	G	N	V	339
CTT	CCT	AAT	ATG	ACT	CAA	GGA	TTC	TGG	GAA	AAT	TCC	ATG	CTA	ACG	GAC	CCA	GGA	AAT	GTT	1098
Q	K	A	V	C	H	P	T	A	W	D	L	G	K	G	D	F	R	I	L	359
CAG	AAA	GCA	GTC	TGC	CAT	CCC	ACA	GCT	TGG	GAC	CTG	GGG	AAG	GGC	GAC	TTC	AGG	ATC	CTT	1158
M	C	T	K	V	T	M	D	D	F	L	T	A	H	H	E	M	G	H	I	379
ATG	TGC	ACA	AAG	GTG	ACA	ATG	GAC	GAC	TTC	CTG	ACA	GCT	CAT	CAT	GAG	ATG	GGG	CAT	ATC	1218
Q	Y	D	M	A	Y	A	A	Q	P	F	L	L	R	N	G	A	N	E	G	399
CAG	TAT	GAT	ATG	GCA	TAT	GCT	GCA	CAA	CCT	TTT	CTG	CTA	AGA	AAT	GGA	GCT	AAT	GAA	GGA	1278
F	H	E	A	V	G	E	I	M	S	L	S	A	A	T	P	K	H	L	K	419
TTC	CAT	GAA	GCT	GTT	GGG	GAA	ATC	ATG	TCA	CTT	TCT	GCA	GCC	ACA	CCT	AAG	CAT	TTA	AAA	1338
S	I	G	L	L	S	P	D	F	Q	E	D	N	E	T	E	I	N	F	L	439
TCC	ATT	GGT	CTT	CTG	TCA	CCC	GAT	TTT	CAA	GAA	GAC	AAT	GAA	ACA	GAA	ATA	AAC	TTC	CTG	1398
L	K	Q	A	L	T	I	V	G	T	L	P	F	T	Y	M	L	E	K	W	459
CTC	AAA	CAA	GCA	CTC	ACG	ATT	GTT	GGG	ACT	CTG	CCA	TTT	ACT	TAC	ATG	TTA	GAG	AAG	TGG	1458
R	W	M	V	F	K	G	E	I	P	K	D	Q	W	M	K	K	W	W	E	479
AGG	TGG	ATG	GTC	TTT	AAA	GGG	GAA	ATT	CCC	AAA	GAC	CAG	TGG	ATG	AAA	AAG	TGG	TGG	GAG	1518

ZBD

Figure 1(B)

M K R E I V G V V E P V P H D E T Y C D 499
 ATG AAG CGA GAG ATA GTT GGG GTG GTG GAA CCT GTG CCC CAT GAT GAA ACA TAC TGT GAC 1578
 P A S L F H V S N D Y S F I R Y Y T R T 519
 CCC GCA TCT CTG TTC CAT GTT TCT AAT GAT TAC TCA TTC ATT CGA TAT TAC ACA AGG ACC 1638
 L Y Q F Q F Q E A L C Q A A K H E G F L 539
 CTT TAC CAA TTC CAG TTT CAA GAA GCA CTT TGT CAA GCA GCT AAA CAT GAA GGC CCT CTG 1698
 H K C D I S N S T E A G Q K L F N M L R 559
 CAC AAA TGT GAC ATC TCA AAC TCT ACA GAA GCT GGA CAG AAA CTG TTC AAT ATG CTG AGG 1758
 L G K S E P W T L A L E N V V G A K N M 579
 CTT GGA AAA TCA GAA CCC TGG ACC CTA GCA TTG GAA AAT GTT GTA GGA GCA AAG AAC ATG 1818
 N V R P L L N Y F E P L F T W L K D Q N 599
 AAT GTA AGG CCA CTG CTC AAC TAC TTT GAG CCC TTA TTT ACC TGG CTG AAA GAC CAG AAC 1878
 K N S F V G W S T D W S P Y A D Q S I K 619
 AAG AAT TCT TTT GTG GGA TGG AGT ACC GAC TGG AGT CCA TAT GCA GAC CAA AGC ATC AAA 1938
 V R I S L K S A L G D K A Y E W N D N E 639
 GTG AGG ATA AGC CTA AAA TCA GCT CTT GGA GAT AAA GCA TAT GAA TGG AAC GAC AAT GAA 1998
 M Y L F R S S V A Y A M R Q Y F L K V K 659
 ATG TAC CTG TTC CGA TCA TCT GTT GCA TAT GCT ATG AGG CAG TAC TTT TTA AAA GTA AAA 2058
 N Q M I L F G E E D V R V A N L K P R I 679
 AAT CAG ATG ATT CTT TTT GGG GAG GAG GAT GTG CGA GTG GCT AAT TTG AAA CCA AGA ATC 2118
 S F N F F V T A P K N V S D I I F R T E 699
 TCC TTT AAT TTC TTT GTC ACT GCA CCT AAA AAT GTG TCT GAT ATC ATT CCT AGA ACT GAA 2178
 V E K A I R M S R S R I N D A F R L N D 719
 GTT GAA AAG GCC ATC AGG ATG TCC CGG AGC CGT ATC AAT GAT GCT TTC CGT CTG AAT GAC 2238
 N S L E F L G I Q P T L G P P N Q P F V 739
 AAC AGC CTA GAG TTT CTG GGG ATA CAG CCA ACA CTT GGA CCT CCT AAC CAG CCC CCT GTT 2299
 S I W L I V F G V V M G V I V V G I V I 759
 TCC ATA TGG CTG ATT GTT TTT GGA GTT GTG ATG GGA GTG ATA GTG GTT GGC ATT GTC ATC 2358
 L I F T G I R D R K K K N K A R S G E N 779
 CTG ATC TTC ACT GGG ATC AGA GAT CGG AAG AAG AAA AAT AAA GCA AGA AGT GGA GAA AAT 2418
 P Y A S I D I S K G E N N P G F Q N T D 799
 CCT TAT GCC TCC ATC GAT ATT AGC AAA GGA GAA AAT AAT CCA GGA TTC CAA AAC ACT GAT 2478
 D V Q T S F * 806
 GAT GTT CAG ACC TCC TTT TAG 2499
 AAAAATCTATGTTTTTCTCTTGTAGGTGATTTTGTGTATGTAAATGTTAATTTTCATGGTATAGAAAATATAAGATGAT 2578
 AAAGATATCATTAAATGTCAAACTATGACTCTGTTTCAGAAAAAAATGTCCAAAGACAACATGGCCAAGGAGAGAGC 2657
 ATCTTCATTGACATTGCTTTTCTGATTTTATTTCTGTCTCTGGATTGACTTCTGTTCTGTTTCTTAATAAGGATTTTGT 2736
 ATTAGAGTATATTAGGGAAGTGTGTATTTGGTCTCACAGGCTGTTTCAGGGATAATCTAAATGTAATGTCTGTTGAAT 2815
 TTCTGAAGTTGAAAACAAGGATATATCATTGGAGCAAGTGTGGATCTTGTATGGAATATGGATGGATCACTTGTAAAG 2894
 ACAGTGCCTGGGAAGTGGTGTAGCTGCAAGGATTGAGAATGGCATGCATTAGCTCACTTTTCAATTAATCCATTGTCAAG 2973
 GATGACATGCTTTCTTACAGTAACCTAGTTCAAGTACTATGGTGAATTTGCCTACAGTGATGTTTGGAAATCGATCATGC 3052
 TTTCTTCAAGGTGACAGGTCTAAAGAGAGAAGAATCCAGGGAACAGGTAGAGGACATTGCTTTTCACTTCCAAGGTGC 3131
 TTGATCAACATCTCCCTGACAACACAAAAGTAGAGCCAGGGGCTCCGTGAATCCCAGAGCATGCCTGATAGAACTC 3210
 ATTTCTACTGTTCTCTAACTGTGGAGTGAATGGAATTCCTCACTGTATGTTTACCCTCTGAAGTGGGTACCCAGTCTCT 3289
 TAAATCTTTTGTATTTGCTCACAGTGTGTTGAGCAGTGTGAGCACAAAGCAGACACTCAATAAATGCTAGATTTACACA 3368
 CTCAAAAAAGGGCGCCGC 3396

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MGAASGRGPGLLLLPLP-----LLLLL-PPQFALALDPGLQPGNFSAD~~E~~AGAQLFAQSYN
MGAASGQGRWFSPPLMLSLVLVLLQP-SFAPALDPGLQPGNFSF~~E~~AGAQLFAESYN
MGAASGQGRWFSPPLMLSLLLLLLPPSPAPALDPGLQPGNFSAD~~E~~AGAQLFADSYN
MGAAPGRGPRLLRPPFPFL-LLLLLLRPPAALTLD~~E~~GPLPGDFA~~E~~AGARLFASSYN

SSAEQVLFSVAASWAHDTNITAENARRQEEAALLSQEFAEWGQKAKELYEPIWQNFTD
SSAEVVMFQSTVASWAHDTNITEENARRQEEAALVSQEFAEVWGKKAKELYESIWNFTD
SSAEVVMFQSTAASWAHDTNITEENARLQEEAALINQEFAEVWGKKAKELYESIWNFTD
SSAEQVLFIRSTAASWAHDTNITAENARRQEEAALLSQEFAEWGRRLSSMTRCGRTSFT

FQLRRIIGAVRTLGSANLPLAKRQQYNALLSNMSRIYSTGKVCLENKATCWSLDPDLTN
SKLRIIGSIRTLGPANLPLAQRQQYNALLSNMSRIYSTGKVCLENKATCWSLDPDLTN
QKLRIIGSVQTLGPANLPLTQRLQYNALLSNMSRIYSTGKVCLENKATCWSLDPDLTN
QSCAGSSGLCAFWFCQAP-GQAAADNSLLSNMSQIYSTGRSASFTR-PAFWSLDPDLNN

ILASSRSYAMLLFAWEGWHNAAGIPLKPLYEDFTALSNEAYKQDGFDTGAYWRSWYNSF
ILASSRSYAKLLFAWEGWHDAVGIPLKPLYQDFTALSNEAYRQDGFSDTGAFWRSWYESF
ILASSRNYAKVLF AWEGWHDAVGIPLRPLYQDFTALSNEAYRQDGFSDTGAYWRSWYESF
ILASSRSYAMLLFAWEGWHNAVGIPLKPLYQEF TALSNEAYRQDGFSDTGAYWRSWYDSF

TFEEDLEHLYQOLEPLYLNLHAFVRRALHRRYGDRYINLRGPIPAHLGDMWAQSWENIY
SFEESLEHIYHQLEPLYLNLHAYVRRALHRRYGDKYVNLRGPIPAHLGDMWAQSWENIY
SFEESLEHIYHQVEPLYLNLHAFVRRALHRRYGDKYINLRGPIPAHLGDMWAQSWENIY
TFEEDLERIYHQLEPLYLNLHAYVRRVLHRRYGDRYINLRGPIPAHLGNMWAQSWESIY

DMVVPPFDKPNLDVSTMLQGGWNATHMFRVAEEFFTSLGLSPMPPEFWAGSMLEKPADG
DMVVPPFDKPNLDVSTMVQKGWNATHMFRVSEEFFTSLGLSPMPPEFWAESMLEKPTDG
DMVVPPFDKPNLDVSTMVQKGWNATHMFRVAEEFFTSLGLSPMPPEFWAESMLEKPADG
DMVVPPFDKPNLDVSTMVQKGWNATHMFRVAEEFFTSLGLLPMPEFWAESMLEKPEDG

REVVCHASAWDFYNRKDFRIKQCTRVMTDQLSTVHHMGHIQYYLQYKDLFVSLRRGANP
REVVCHASAWDFYNRKDFRIKQCTRVMEQLATVHHMGHVQYYLQYKDLHVSLLRRGANP
REVVCHASAWDFYNRKDFRIKQCTRVMTDQLSTVHHMGHVQYYLQYKDLHVSLLRRGANP
REVVCHASAWDFYNRKDFRIKQCTQVTMDQLSTVHHMGHVQYYLQYKQDFVSLRR--ANP

Figure 2 (B)

ace-2
hu-ACET
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rb-ACET
hu-ACE
mu-ACE
rat-ACE
rb-ACE

GFHEAIGDVLALS SVSTFEHLHKIGLLDRVTNDTESDINYLKMALEKIAFLPFGYLVLDQW
GFHEAIGDVLALS SVSTFAHLHKIGLLDHVTNDIESDINYLKMALEKIAFLPFGYLVLDQW
GFHEAIGDVLALS SVSTFAHLHKIGLLDRVANDIESDINYLKMALEKIAFLPFGYLVLDQW
GFHEAIGDVLALS SVSTFAHLHKIGLLDHVTNDTESDINYLKMALEKIAFLPFGYLVLDQW

ace-2
hu-ACET
mu-ACET
rb-ACET
hu-ACE
mu-ACE
rat-ACE
rb-ACE

RWGVFSGRTPPSRYNFDWWYLRTKYQGICPPVTRNETHFDAGAKFHVFNVTPIRYFVSF
RWGVFSGRTPPSRYNFDWWYLRTKYQGICPPVARNETHFDAGAKFHIENVTPIRYFVSF
RWGVFSGRTPPSRYNFDWWYLRTKYQGICPPVARNETHFDAGAKFHIENVTPIRYFVSF
RWGVFSGRTPPSRYNFDWWYLRTKYQGICPPVARNETHFDAGAKFHIENVTPIRYFVSF

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mu-ACE
rat-ACE
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-----MGQGWATAGLPSSLFLLLC
-----MGQGWATPGLPSFLFL----LC
-----MGQGWAPGLPSLLLLLCCGHSLL
VLQFQFHEALCKEAGYEGPLHQCDIYRSTKAGAKLRKVLQAGSSRPWQEVLDKDMVGLDAL
VLQFQFHQALCKEAGHQGFLHQCDIYQSTQAGAKLKQVLQAGCSRWPQEVLDKLVGSDAL
VLQFQFHQALCKEAGHQGFLHQCDIYQSTKAGAKLQVLQAGCSRWPQEVLDKLVGSDAL
VLQFQFHQALCKEAGHQGFLHQCDIYQSTRAGAKLRAVLQAGCSRWPQEVLDKDMVGLDAL

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-----MSSSWLLLSLVAVTAA---QSTIEEQAKTFL
YGHPLLVFSQEQVTVTHGTSSQATTSSQTTTHQATAHQTSAQSFNLVTDAAEASKFV
CGHLLLVLSQVATDHVTANQGITNQATTSQTTHQATIDQTTQI-FNLETDEAKADRFV
VPSRVAARRVTVNQGTTSQATTTSKATTSIRATTHQTTHQATTSQSFNLVTDAAEASRFV
DAQPLLLKYFQPVTVLQEQNQNGEVLGWPEYQWHFPLPDNYPEG-IDLVTDEAEASKFV
DAKALLEYFQPVSVQWLEEQNQNGEVLGWPEYQWRPPLPDNYPEG-IDLETDEAKADRFV
DASALMEYFQPVSVQWLEEQNQNGEVLGWPEYQWRPPLPDNYPEG-IDLETDEAKANRFV
DAQPLLDYFQPVTVLQEQNERNGEVLGWPEYQWRPPLPNNYPEG-IDLVTDEAEASRFV
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DKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNAGDKWSAFLKEQSTLAQMYFLOEIQ
EEYDRTSQVWVNEYAEANWNYNTNITETSKILLQKNMQIANHTLKYGTQARKFDVNLQ
EEYDRTAQVLLNEYAEANWNYNTNITIEGSKILLEKSTEVSNHTLKYGTQARKFDVSNFQ
EEYDRSFQAVWVNEYAEANWNYNTNITTEASKILLQKNMQIANHTLTYGNWARRFDVSNFQ
EEYDRTSQVWVNEYAEANWNYNTNITETSKILLQKNMQIANHTLKYGTQARKFDVNLQ
EEYDRTAQVLLNEYAEANWNYNTNITIEGSKILLEKSTEVSNHTLKYGTQARKFDVSNFQ
EEYDRTAQVLLNEYAEANWNYNTNITIEGSKILLQKNKEVSNHTLKYGTWAKTFDVSNFQ
EEYDRSFQAVWVNEYAEANWNYNTNITTEASKILLQKNMQIANHTLTYGNWARRFDVSNFQ
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NLTVKLQALQALQONGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQECLELLEPGLN
NTTIKRIIKKVQDLERAAALPAQEEYNYKILLDMETTSVATVCHPNG--SCLQLEPDLT
NSSIKRIIKKLQNLDRAVLPPKELEEYNYQILLDMETTSVATVCHPNG--SCLQLEPDLT
NATSKRIIKKVQDLQRAVLPPKELEEYNYQILLDMETTSVATVCHPNG--SCLQLEPDLT
NTTIKRIIKKVQDLERAAALPAQEEYNYKILLDMETTSVATVCHPNG--SCLQLEPDLT
NSSIKRIIKKLQNLDRAVLPPKELEEYNYQILLDMETTSVATVCHPNG--SCLQLEPDLT
NSTIKRIIKKVQDLQRAVLPPKELEEYNYQILLDMETTSVATVCHPNG--SCLQLEPDLT
NATSKRIIKKVQDLQRAVLPPKELEEYNYQILLDMETTSVATVCHPNG--SCLQLEPDLT
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EIMANSIDYNERLWAWESWRSEVGKQLRPLYEYVVLKNEMARANHYEDYGDYWRGDYEV
NVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAARLNGYVDAGDSWRSMYET
NMMATSRKYEDLLWAWKSWRDKVGRAILPFPKYVEFSNKIAKLNGYTDAGDSWRSLYES
NLMATSRKYEDLLWVWTSWRDKVGRAILPFPKYVEFTNKAARLNGYVDAGDSWRSMYET
NVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAARLNGYVDAGDSWRSMYET
NMMATSRKYEDLLWAWKSWRDKVGRAILPFPKYVEFSNKIAKLNGYTDAGDSWRSLYES
NIMATSRKYEDLLWVWTSWRDKVGRAILPFPKYVEFTNKAARLNGYVDAGDSWRSMYET
NLMATSRKYEDLLWVWTSWRDKVGRAILPFPKYVEFTNKAARLNGYVDAGDSWRSMYET
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[illegible]

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HUM_tACE -----
HUM_ace ----- MGAASGRRGPGLLLPPLLLLLPFPQPALALDPGLQPGNFSADEAGAQLFAQSYNSSAEQV
DROME_ace -----
ace-2 -----
CE_ace -----

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HUM tACE -----
HUM ACE      LFQSVAAASWAHDTNITAENARRQEEAALLSQEFAEAWGQKAKELYEPIWQNFTDPQLRRI
DROME ACE    -----
ace-2        -----
CE ACE       -----

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HUM_tACE	-----
HUM_ace	IGAVRTLGSANLPLAKRQQYNALLSNMSRIYSTAKVCLPNKTATCWSLDPDLTNILASSR
DROME_ace	-----
ace-2	-----
CE_ace	-----

HUM_tACE	-----
HUM_ace	SYAMLLFAWEGWHNAAGIPLKPLYEDFTALSNEAYKQDGFDTGTAYWRSWYNSPTFEDDL
DROME_ace	-----
ace-2	-----
CE_ace	-----

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HUM_tACE      -----
HUM_ACE       EHLYQQLEPLYLNLHAFVRRALHRRYGDRYINLRGPIPAHL LGDMWAQSWENIYDMVVPF
DROME_ACE     -----
ace-2         -----
CE ACE        -----

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HUM_tACE	-----
HUM_ACE	PDKPNLDVTSTMLQQGWNATHMFRVAEEFFTSLELSPMPPEFWEGSMLEKPADGREVVCH
DROME_ACE	-----
ace-2	-----
CE ACE	-----

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HUM_tACE      -----
HUM_ACE       ASAWDFYNRKDFRIKQCTRVMTDQLSTVHHMGHIQYYLQYKDLPVSLRRGANPGFHEAI
DROME_ACE     -----
ace-2         -----
CE ACE        -----

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HUM_tACE -----
HUM_ACE      GDVLALS SVSTPEHLHKIGLLDRVTNDTESDIN YLLKMALEKIAFLPFGYLVDQWRWGVFS
DROME_ ACE   -----
ace-2        -----
CE ACE       -----MKFHI LLLLLLV

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HUM_tACE      -----
HUM_ ACE      GRTPPSRYNFDWWYLRTKYQGICPPVTRNETHFDAGAKFHVPNVTPYIRYFVSFVLQFQF
DROME_ ACE    -----
ace-2         -----
CE ACE        GACLPVFTQEIKPKPELLPADEAPKDPEAVFSEGEPELTDALDTPKNGSVVPVPEPEPKP

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SECRET

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HUM_tACE      -----MGQGWATAGTAPLSSLLFLLLCYGHPLL
HUM_ ACE      HEALCKEAGYEGPLHQCDIYRSTKAGAKLRKVLQAGSSRPWQEVLKDMVGLDALDAQPLL
DROME_ ACE    -----
ace-2         -----
CE_ ACE      EPEPEPEPKPEPEPSPTPEPEPAIKFDNIESEDYGDVAETAASTQPDDELNTEVIEQLVDT

HUM_tACE      VPSQEASQQVTVTHTGTSSQATTSSQTTTHQATAHQTSAQSPNLVTDDEAEASKFVEEYDRT
HUM_ ACE      KYFQPVTOQLQEONQONGEVLGWPEYQWHPPLPDNYPEG-IDLVTDEAEASKFVEEYDRT
DROME_ ACE    -----MRLFLLLALLATLAVTQALVKEEIQAKEYLENLNKE
ace-2         -----MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHE
CE_ ACE      FLNTGSIASNKTNKGPFVAFNPVAQALVNSSNYWKTNDLQAPGSIKDEEKLRSWLAGYEAE
               . * : : :

HUM_tACE      SQVWVNEYAEANWNYNTNITTETSKILLQKNMQIANHTLKYGTQARKFDVNQLQNTTIKR
HUM_ ACE      SQVWVNEYAEANWNYNTNITTETSKILLQKNMQIANHTLKYGTQARKFDVNQLQNTTIKR
DROME_ ACE    LAKRTNVETEAAWAYGSNITDENEKKKNEISAEIAKFMKEVASDITTKFQWRSYQSEDLKR
ace-2         AEDLFYQSSLASWNYNTNITEENVQNMNNAAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKL
CE_ ACE      AIKVLREVALSGWRVFNDAFSLKLALDEANVLTMFVRSTSMQAKQFDMASVTDEKVMR
               : * * . : : : : : : : : : : : : : : :

HUM_tACE      IIKKVQDLERAALPAQELEEYNKILLDMETTYSVATVCHPNGS---CLQLEPDLTNVMAT
HUM_ ACE      IIKKVQDLERAALPAQELEEYNKILLDMETTYSVATVCHPNGS---CLQLEPDLTNVMAT
DROME_ ACE    QFKALTKLGAAALPEDDYAELLDTLSAMESNFAKVVCDDYKSTKCDLALDPEIEEVISK
ace-2         QLQALQONGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQE-CLLEPGLNEIMAN
CE_ ACE      QLGYSVFEGMSALAPSRFADYSQAQAALNRDSKDISTCDKDVPPP-CALQKIDMDSIFRN
               : : : * . : : : : : : : : : : : : : : :

HUM_tACE      SRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAARLNGYVDAGDSWRSMYETP----
HUM_ ACE      SRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAARLNGYVDAGDSWRSMYETP----
DROME_ ACE    SRDHEELAYWREFYDKAGTAVRSQFERYVELNTKAALNNFTSGAEAWLDEYEDD----
ace-2         SLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDG
CE_ ACE      EKDASRLQHLWVSYVTAIAKSK-PSYNNIITISNEGAKLNGFANGGANWRSAFDMSS--K
               . . . * : . : : : : : * : * : . . * . : :

HUM_tACE      -----SLEQDLERLFOELQPLYLNLHAYVRRALHRHYG-AQHINLEGP I PAHLLGNMWA
HUM_ ACE      -----SLEQDLERLFOELQPLYLNLHAYVRRALHRHYG-AQHINLEGP I PAHLLGNMWA
DROME_ ACE    -----TFEQLEDIFADIRPLYQQIHGYVFRRLRKHYG-DAVSETGP I PMHLLGNMWA
ace-2         YDYSRGQLIEDVEHTFEEKPLPYEHLHAYVRAKLNNAY--PSYISPIGCLPAHLLGDMWG
CE_ ACE      VHKAEFDLNKQIDKIYSTIQPFYQLLHAYMRRQLAGIYSNPVGLSKDGP I PAHLFGSLDG
               : : : : : : : * : * * * * : : * : * * * : : .

HUM_tACE      QTWSNIYDLVVPFPSA--PSMDTTEAMLKQGWTPRRMFKEADDFFTSLGLLPVPPEFWNK
HUM_ ACE      QTWSNIYDLVVPFPSA--PSMDTTEAMLKQGWTPRRMFKEADDFFTSLGLLPVPPEFWNK
DROME_ ACE    QQWSEIADIVSPFPEK--PLVDVSAEMEKAQYATPLKMFQMGDDFTSMNLTKLPQDFWDK
ace-2         RFWTNLSLTVPEFGQK--PNIDVTDAMVDQAWDAQRIKFEAEKFVSVGLPNMTQGFWEN
CE_ ACE      GDWSAHYEQTKPFEESESETPEAMLSAFNTQYNTTKMFVTAYRYFKSAGFPHLPKSYWTS
               * : . . * * . : : : : : * : : : : * * : : . : * .

HUM_tACE      SMLEKPTDGREVVCHAS-AWDFYNGKDFRIKQCTTVNLEDLVVAHHEMGHIQYFMQYKDL
HUM_ ACE      SMLEKPTDGREVVCHAS-AWDFYNGKDFRIKQCTTVNLEDLVVAHHEMGHIQYFMQYKDL
DROME_ ACE    SIIEKPTDGRDLVCHAS-AWDFYLIDVRIKQCTRTVTDQDLFTVHHELGHIIQYFLQYQHQ
ace-2         SMLTDPGNVQKAVCHPT-AWDLGKG-DFRILMCTKVMTMDDFLTAFHEMGHIQYDMAYAAQ
CE_ ACE      SIFAR-VWSKDMIHPAAALDMRAPNDFRVKACAQLGEPDEQAHSLLVQTYYYQYLYKQD
               * : : : : * * : : : : * : : : : : : : : : : * * : : : *

HUM_tACE      PVALREGANPGFHEAIGDVLALS SVSTPKHLHSLNLLSSEGGSD--EHDINFLMKMALDKI
HUM_ ACE      PVALREGANPGFHEAIGDVLALS SVSTPKHLHSLNLLSSEGGSD--EHDINFLMKMALDKI
DROME_ ACE    PFVYRTGANPGFHEAVGDVLSLSVSTPKHLEKIGLLKDYVRDD--EARINQLFLTALDKI
ace-2         PFLLRQANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDN-ETEINFLKQALTIV
CE_ ACE      SLLFREQASPVITDAIANAF AHLSTNPHYLYSQKLVPSHLDIKDSVIINKLYKESLESF
               . . * * . : : : : : : : : : : * : : : : * * * : : *

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60693 = 60693

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HUM_tACE      -SSVPYIRYFVSFIIQFQFHEALCQAAGHTG-----PLHKCDIYQSKEAGQRLATAMKL
HUM_ACE       -SSVPYIRYFVSFIIQFQFHEALCQAAGHTG-----PLHKCDIYQSKEAGQRLATAMKL
DROME_ace     -ADVYLYRLYLSFIIQFQFYKSACIKAGQYDPDNVELPLDNCDIYGSAAAFHNMLSM
ace-2         -NDYSFIRYYTRTLYQFQFQEALCQAAKHEG-----PLHKCDISNSTEAGQKLFNMLRL
CE_ACE        QVHSPATRTLISYVLKFQIKALCQRELFWL-----SEGCILSEDTK---EKLRETMKL
              *   *   *   *   *   *   *   *   *   *   *   *   *   *   *

```

```

HUM_tACE      GFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTEN-----
HUM_ace       GFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTEN-----
DROME_ace     GASKPWPDALEAFNGERIMSGKAI AEYFEPLRVWLEAEN-----
ace-2        GKSEPWTTLAENVVGAKNMNVRPLLNYFEPLFTWLKDNQKNSSFVGWSTDWSPYADQSIKV
CE_ace       GSSITWLKALEMISGKGELDAQPLLEYEPLINWLRTN-----
              * * * * * * * * * * * * * * *

```

```

HUM_tACE      -ELHGEKLGWPQYNWTPNSAR-----
HUM_ACE       -ELHGEKLGWPQYNWTPNSAR-----
DROME_ACE     -IKNVHIGWTTTSNKCVCSS-----
ace-2         RISLSKALGDKAYEWNNDNEMYLFRRSSVAYAMRQYFLKVKNQMILFGEEDVRVANLKPRIS
CE_ACE        -EIDQVVVGWDGEGTPTFVEEIPKTRQPGDGGNGLPSEDRVAFPGGE-----
               **

```

```

HUM_tACE      -----SEGPLPDSGRVSFLGLDLDAQQARVG-----Q
HUM_ ACE      -----SEGPLPDSGRVSFLGLDLDAQQARVG-----Q
DROME_ ACE    -----
ace-2         FNFFVTAPKNVSDIIIPRTEVEKAIRMSRSRINDAFRLDNSLEFLGIQPTLGPPNQPPVS
CE ACE        -----CVNGQECLLDSHCNGTICVCNDGLYTLTEIGNTFN---CVPGN

```

```

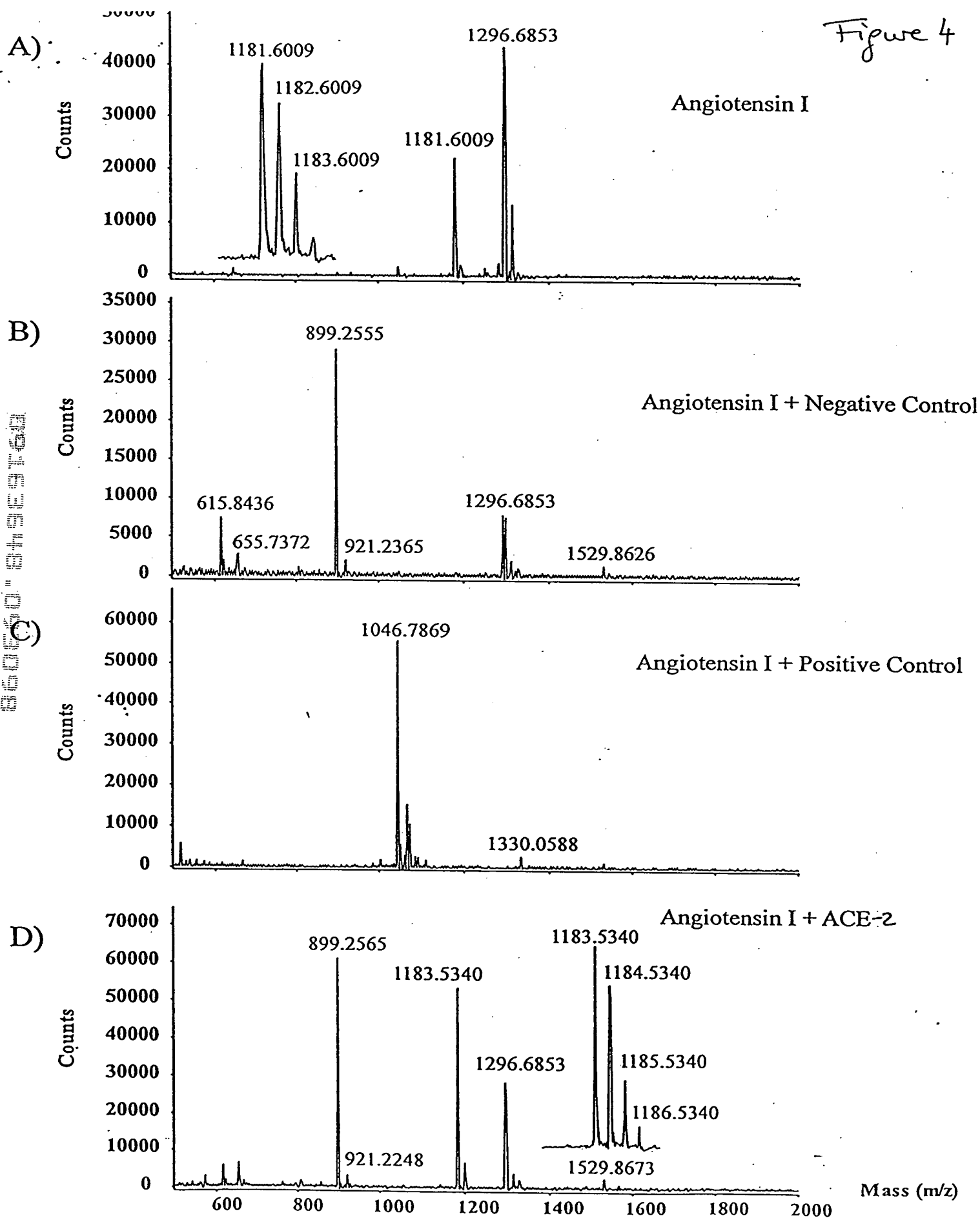
HUM tACE      WLLFLGLGIALLVATLGLSQR LFS-IRHR-----SLHRHSHGPGQFGSEVE
HUM ACE       WLLFLGLGIALLVATLGLSQR LFS-IRHR-----SLHRHSHGPGQFGSEVE
DROME ACE     -----
ace-2         IWLIVFGVVMGVIVVGIVILFTGILRDRKKKNKARS GENPYASIDISKGENNPGFQNTDD
CE ACE        PADSGFGDGKGGLVIGLFNN ETTPEPSAEPEP--TAKTTTKMPPRVRAATSPFSLYLTV

```

HUM_tACE	LRHS----
HUM_ ACE	LRHS----
DROME_ ACE	-----
ace-2	VQTSFN--
CE ACE	LLIIYFAL

TMD

Figure 4



acehomo2 175 (3.292) Cm (103:276) 1: TOF MSMS 395.40ES+ 310

660660" 849E9T60

Figure 5

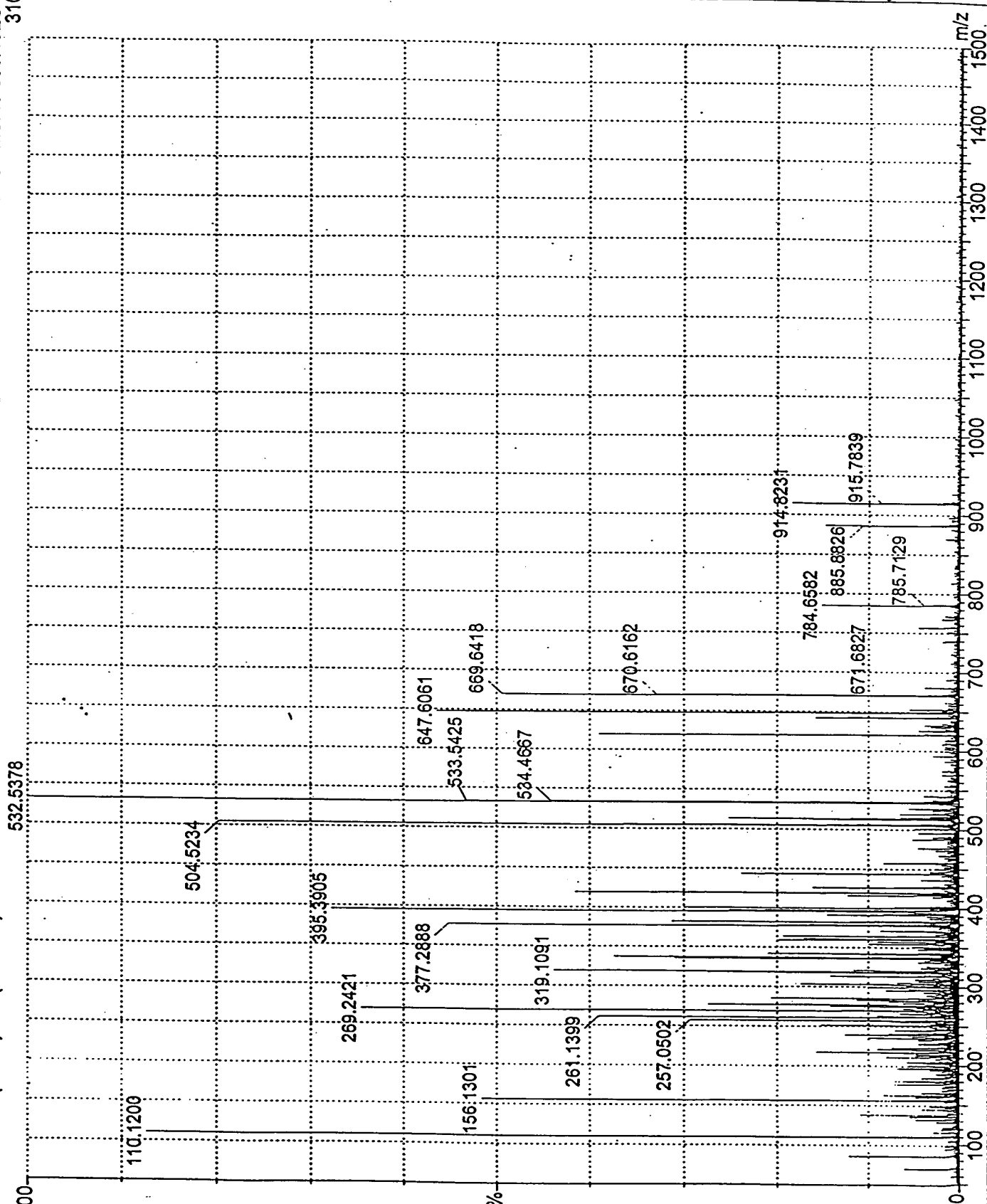
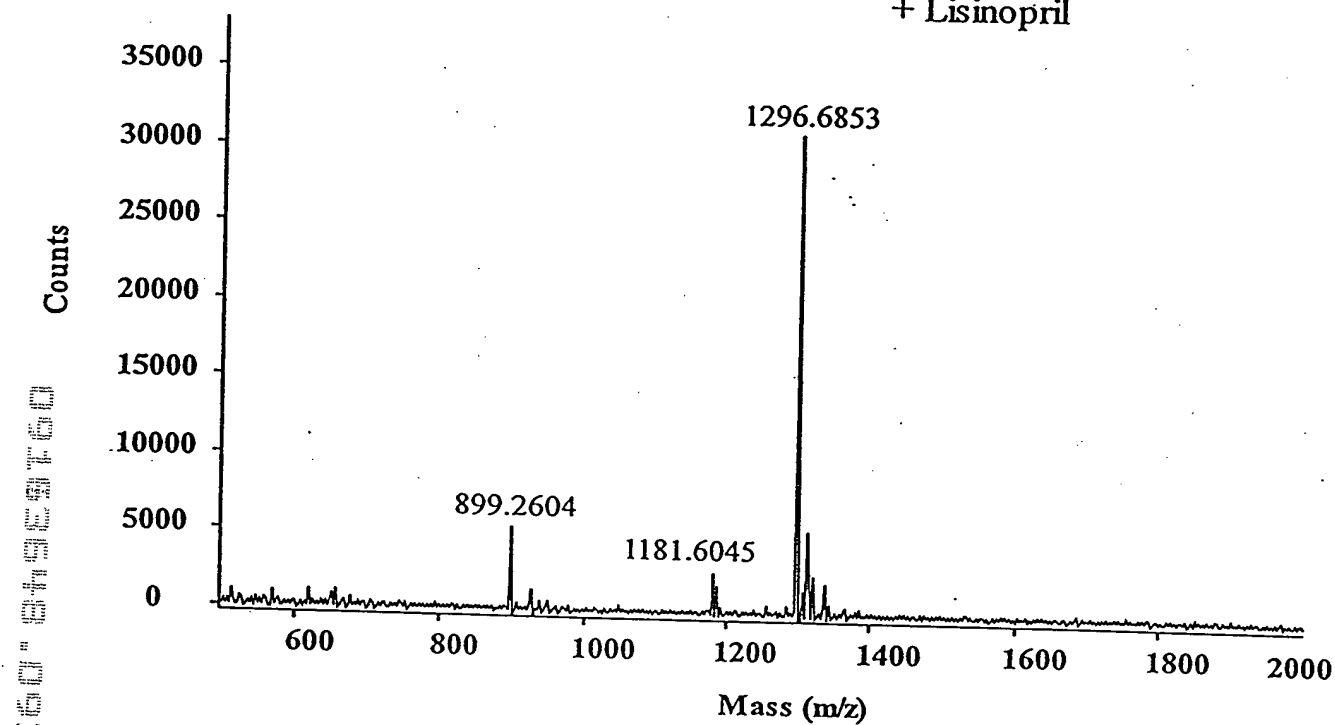


Figure 6

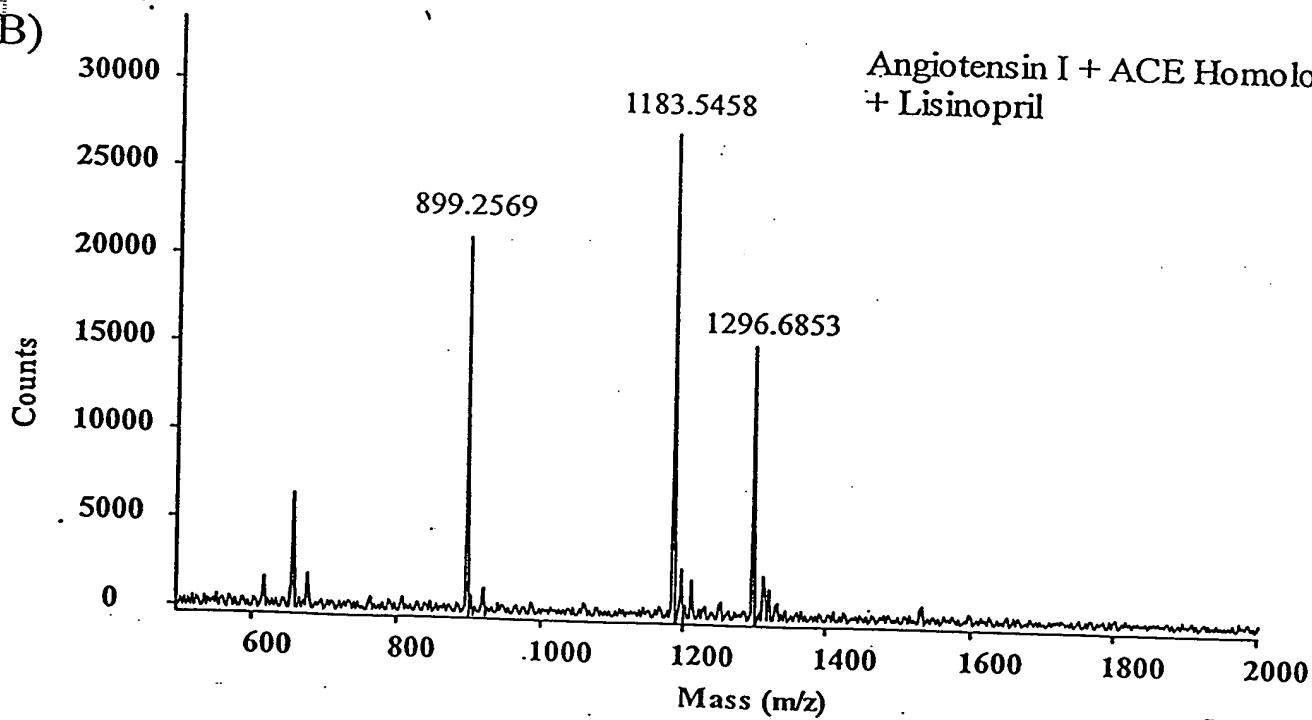
A)

Angiotensin I + Positive Control
+ Lisinopril



B)

Angiotensin I + ACE Homolog
+ Lisinopril



Angiotensin I conversion to products

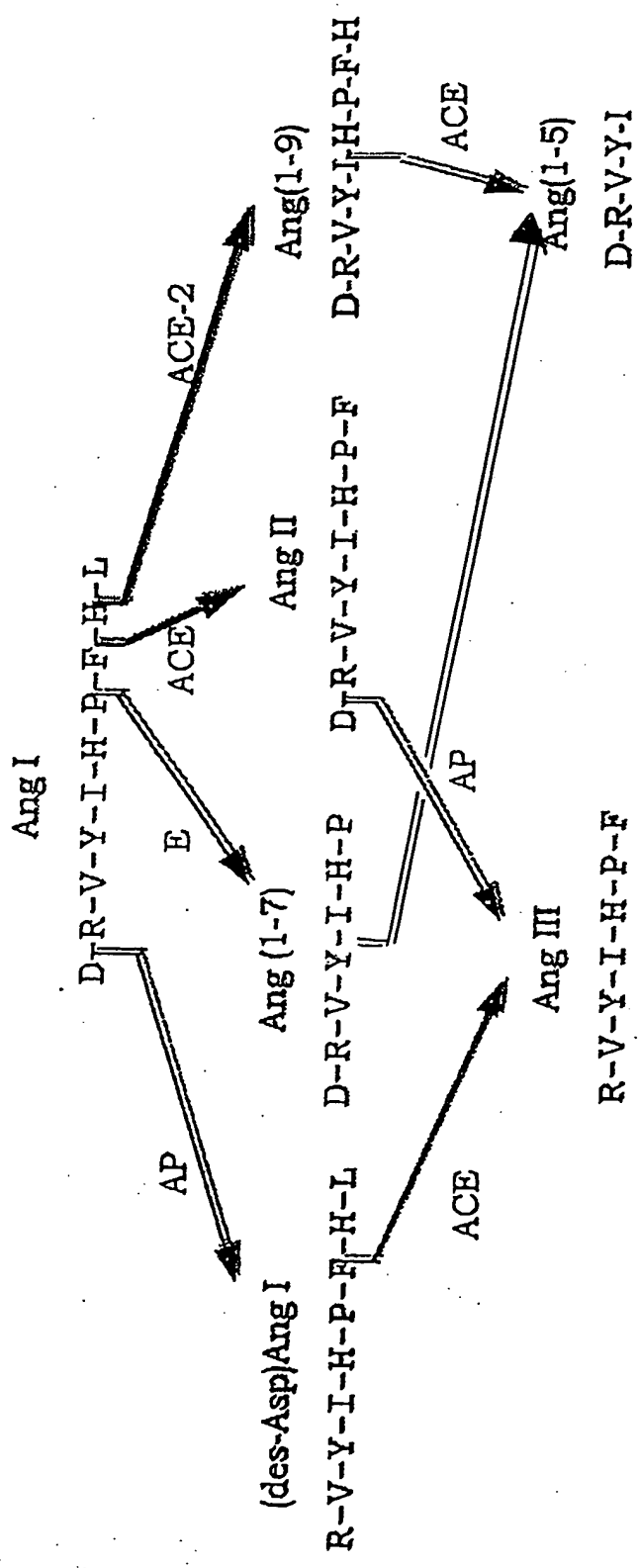


Figure 7.